

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	20	100.0	20	11	US-09-920-671-80	Sequence 80, Appl
C	2	13.8	69.0	25	US-10-098-263B-59092	Sequence 59092, A
	3	13.6	68.0	27	US-10-310-734-35	Sequence 35, Appl
	4	13.6	68.0	27	US-10-123-101-35	Sequence 35, Appl
C	5	13.6	68.0	47	US-10-349-143-1075	Sequence 1075, Ap
	6	13.6	68.0	47	US-10-349-143-1167	Sequence 1167, Ap
	7	13.6	68.0	50	US-09-909-320-110	Sequence 110, App
	8	13.6	68.0	50	US-09-909-088B-110	Sequence 110, App
	9	13.6	68.0	50	US-09-905-291A-110	Sequence 110, App
	10	13.6	68.0	50	US-09-902-853-110	Sequence 110, App
11	13.6	68.0	50	US-09-907-824-110	Sequence 110, App	
12	13.6	68.0	50	US-09-907-841-110	Sequence 110, App	
13	13.6	68.0	50	US-09-904-011-110	Sequence 110, App	
14	13.6	68.0	50	US-09-905-742-110	Sequence 110, App	
15	13.6	68.0	50	US-09-906-838-110	Sequence 110, App	

```

RESULT 2
US-10-098-263B-59092/c
; Sequence 59092, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

```

; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-59092

Query Match 69.0%; Score 13.8; DB 15; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGTCTCGATCTCCAT 19
|||||
Db 21 GGTGTCTGTCTCCAT 5

RESULT 3

US-10-310-734-35
; Sequence 35, Application US/10310734
; Publication No. US20030232324A1
; GENERAL INFORMATION:
; APPLICANT: POLO, John
; APPLICANT: PERRI, Silvia
; APPLICANT: THUDIUM, Kent
; APPLICANT: TANG, Zegun
; TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES
; FILE REFERENCE: CHIR-17924/02US (2300-17924.20)
; CURRENT APPLICATION NUMBER: US/10/310,734
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 10/123,101
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VE2F
US-10-310-734-35

Query Match 68.0%; Score 13.6; DB 12; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
|||||
Db 7 CAGGGGACTCCATCACCATG 26

RESULT 4

US-10-123-101-35
; Sequence 35, Application US/10123101
; Publication No. US20030148262A1
; GENERAL INFORMATION:
; APPLICANT: POLO, John
; APPLICANT: PERRI, Silvia
; APPLICANT: THUDIUM, Kent
; TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES
; FILE REFERENCE: 2300-17924 / PP17924.002
; CURRENT APPLICATION NUMBER: US/10/123,101
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/295,451
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 27
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VE2F
US-10-123-101-35

Query Match 68.0%; Score 13.6; DB 13; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
|||||
Db 7 CAGGGGACTCCATCACCATG 26

RESULT 5

US-10-349-143-1075/c
; Sequence 1075, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1075
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2027-296 : polymorphic base A or G
US-10-349-143-1075

Query Match 68.0%; Score 13.6; DB 12; Length 47;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
|||||
Db 46 CAGATGTATCCATCTGCATG 27

RESULT 6

US-10-349-143-1167
; Sequence 1167, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614

[REDACTED]

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E-mail: shawn.walker@utoronto.ca

;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 110
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: oligonucleotide probe
US-09-909-088B-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCGATCTCCATG 20
||| ||||| |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 9
US-09-905-291A-110
; Sequence 110, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,291A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 110
;; LENGTH: 50
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: oligonucleotide probe
US-09-905-291A-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCGATCTCCATG 20
||| ||||| |||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 10
US-09-902-853-110
; Sequence 110, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi


```
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-853-110
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Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;

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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGTCGATCTCCATG 20
   |||||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 11
US-09-907-824-110
; Sequence 110, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-824-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. NO. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
||| ||||| ||||| |||||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 12

US-09-907-841-110
; Sequence 110, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 110
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-841-110

Query Match 68.0%; Score 13.6; DB 10; Length 50;
Best Local Similarity 80.0%; Pred. NO. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
||| ||||| ||||| |||||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 13

US-09-904-011-110
; Sequence 110, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 110
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-011-110

Query Match 68.0%; Score 13.6; DB 11; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
||| ||||| ||||| |||||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 14
US-09-906-742-110
Sequence 110, Application US/09906742
Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 110
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-906-742-110

Query Match 68.0%; Score 13.6; DB 11; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
||| ||||| ||||| |||||
Db 24 CAAGTGTCTCGATGTGGATG 43

RESULT 15
US-09-906-838-110
Sequence 110, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

Search completed: January 28, 2004, 19:46:33
Job time : 270 secs

APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 110
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-906-838-110

Query Match 68.0%; Score 13.6; DB 11; Length 50;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCGATCTCCATG 20
Db 24 CAAGTGTCTCGATGTGGATG 43

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OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:37:22 ; Search time 76 Seconds
(without alignments)
116.153 Million cell updates/sec

Title: US-09-920-671-80

Perfect score: 20

Sequence: 1 caggtgtctgcgtctccatg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 809828

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	13.8	69.0	21	4	US-09-099-053-24	Sequence 24, Appl
C 2	13.6	68.0	30	4	US-09-638-649-9	Sequence 9, Appl
C 3	13.6	68.0	47	4	US-09-422-978-1075	Sequence 1075, Ap
C 4	13.6	68.0	47	4	US-09-422-978-1167	Sequence 1167, Ap
C 5	13.6	68.0	61	3	US-09-023-228B-41	Sequence 41, Appl
C 6	13.6	68.0	61	4	US-09-163-025B-41	Sequence 41, Appl
C 7	13.6	68.0	61	4	US-10-037-282-41	Sequence 41, Appl
C 8	13.2	66.0	39	1	US-08-431-896B-5	Sequence 5, Appl
C 9	13.2	66.0	60	3	US-09-023-228B-36	Sequence 36, Appl
C 10	13.2	66.0	60	4	US-09-163-025B-36	Sequence 36, Appl
C 11	13.2	66.0	60	4	US-10-037-282-36	Sequence 36, Appl
C 12	13.2	66.0	64	1	US-08-431-896B-7	Sequence 7, Appl
C 13	13.2	66.0	66	1	US-08-431-896B-4	Sequence 4, Appl
C 14	13	65.0	66	4	US-09-209-525-19	Sequence 19, Appl
C 15	12.8	64.0	20	3	US-09-311-260-98	Sequence 98, Appl
C 16	12.8	64.0	47	4	US-09-422-978-2736	Sequence 2736, Ap
C 17	12.8	64.0	47	4	US-09-422-978-2965	Sequence 2965, Ap
C 18	12.6	63.0	20	4	US-09-183-636-3	Sequence 3, Appl
C 19	12.6	63.0	21	2	US-08-117-952-688	Sequence 688, App
C 20	12.6	63.0	26	1	US-08-261-206A-67	Sequence 67, Appl
C 21	12.6	63.0	27	3	US-08-776-971-83	Sequence 83, Appl
C 22	12.6	63.0	42	2	US-08-379-057-54	Sequence 54, Appl
C 23	12.6	63.0	63	1	US-08-198-431-38	Sequence 38, Appl
C 24	12.6	63.0	63	1	US-08-564-955-38	Sequence 38, Appl
C 25	12.6	63.0	63	2	US-08-537-874-38	Sequence 38, Appl
C 26	12.6	63.0	63	3	US-08-621-859-38	Sequence 38, Appl
C 27	12.6	63.0	63	3	US-09-100-856A-38	Sequence 38, Appl

C 28	12.6	63.0	63	3	US-09-075-511-38	Sequence 38, Appl
C 29	12.6	63.0	63	3	US-09-099-015-38	Sequence 38, Appl
C 30	12.6	63.0	63	3	US-09-232-863-38	Sequence 38, Appl
C 31	12.6	63.0	63	3	US-09-133-508A-38	Sequence 38, Appl
C 32	12.6	63.0	63	3	US-09-165-060-38	Sequence 38, Appl
C 33	12.6	63.0	63	3	US-09-501-698-38	Sequence 38, Appl
C 34	12.6	63.0	63	4	US-09-240-310-38	Sequence 38, Appl
C 35	12.6	63.0	63	4	US-09-590-778-38	Sequence 38, Appl
C 36	12.6	63.0	63	4	US-09-477-763-38	Sequence 38, Appl
C 37	12.6	63.0	63	4	US-09-590-774-38	Sequence 38, Appl
C 38	12.6	63.0	63	4	US-09-619-550-38	Sequence 38, Appl
C 39	12.6	63.0	63	4	US-09-240-734-38	Sequence 38, Appl
C 40	12.6	63.0	63	4	US-09-231-253-38	Sequence 38, Appl
C 41	12.6	63.0	63	4	US-09-724-958-38	Sequence 38, Appl
C 42	12.6	63.0	63	4	US-09-696-322-38	Sequence 38, Appl
C 43	12.6	63.0	63	4	US-09-717-391-38	Sequence 38, Appl
C 44	12.6	63.0	63	4	US-09-696-313-38	Sequence 38, Appl
C 45	12.6	63.0	63	4	US-09-240-307-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-099-053-24/c
; Sequence 24, Application US/09099053
; Patent No. 6388063
; GENERAL INFORMATION:
; APPLICANT: Greg Plowman
; APPLICANT: Susan Onrust
; APPLICANT: David Markby
; APPLICANT: Sara Courtneidge
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SAD RELATED DISORDERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,053
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/049,914
; FILING DATE: June 18, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 235/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-053-24

Query Match 69.0%; Score 13.8; DB 4; Length 21;

Best Local Similarity 88.2%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GTGTCTCGATCTCCATG 20
Db 21 GTGTCTCGATCTCCCTG 5

RESULT 2
US-09-638-649-9/c
; Sequence 9, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primers
US-09-638-649-9

Query Match 68.0%; Score 13.6; DB 4; Length 30;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGCTCTCGATCTCCATG 20
Db 22 CAGGTGCTCTCGAGATCTTG 3

RESULT 3
US-09-422-978-1075/c
; Sequence 1075, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1075
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2027-296 : polymorphic base A or G
US-09-422-978-1075

Query Match 68.0%; Score 13.6; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGCTCTCGATCTCCATG 20
Db 46 CAGATGTATCCATCTGCATG 27

RESULT 4
US-09-422-978-1167
; Sequence 1167, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1167
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-2085-172 : polymorphic base C or T
US-09-422-978-1167

Query Match 68.0%; Score 13.6; DB 4; Length 47;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGCTCTCGATCTCCATG 20
Db 2 CAGATGTATCCATCTGCATG 21

RESULT 5
US-09-023-228B-41
; Sequence 41, Application US/09023228B
; Patent No. 6140490
; GENERAL INFORMATION:
; APPLICANT: BIESECKER, GREGORY
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Place #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,228B
; FILING DATE: 12-FEBRUARY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/01739
; FILING DATE: 30 JAN 1997
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/595,335
FILING DATE: 1 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson, Esq.
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX50/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F modified

US-09-023-228B-41

Query Match 68.0%; Score 13.6; DB 3; Length 61;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|||:|:|:|:|:|:|:|:|:|:
Db 13 CGGGCGUCUCGAGCUCUAUG 32

RESULT 6

US-09-163-025B-41
Sequence 41, Application US/09163025B
Patent No. 6395888

GENERAL INFORMATION:
APPLICANT: Nexstar Pharmaceuticals, Inc.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: NEX 50 CIP2
CURRENT APPLICATION NUMBER: US/09/163,025B
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 09/023,228
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: PCT/US97/01739
PRIOR FILING DATE: 1997-01-30
NUMBER OF SEQ ID NOS: 198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 61
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Completely
OTHER INFORMATION: Synthesized Nucleic Acid
NAME/KEY: modified base
LOCATION: (1)..(61)
OTHER INFORMATION: All c's and u's are 2'-F

US-09-163-025B-41

Query Match 68.0%; Score 13.6; DB 4; Length 61;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|||:|:|:|:|:|:|:|:|:|:
Db 13 CGGGCGUCUCGAGCUCUAUG 32

RESULT 7

US-10-037-282-41
Sequence 41, Application US/10037282
Patent No. 6566343

GENERAL INFORMATION:
APPLICANT: BIESECKER, GREGORY

APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: NEX 50 CIP 2 CON
CURRENT APPLICATION NUMBER: US/10/037,282
CURRENT FILING DATE: 2002-01-03
PRIOR APPLICATION NUMBER: 09/163,025
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 08/595,335
PRIOR FILING DATE: 1996-02-01
PRIOR APPLICATION NUMBER: PCT/US97/01739
PRIOR FILING DATE: 1997-01-30
NUMBER OF SEQ ID NOS: 198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 61
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
OTHER INFORMATION: all pyrimidines are 2'F

US-10-037-282-41

Query Match 68.0%; Score 13.6; DB 4; Length 61;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGGTGTCTCGATCTCCATG 20
|||:|:~|:|:|:|:|:|:|:|:|:
Db 13 CGGGCGUCUCGAGCUCUAUG 32

RESULT 8

US-08-431-896B-5/c
Sequence 5, Application US/08431896B
Patent No. 5773244
GENERAL INFORMATION:
APPLICANT: Ares, Manuel, Jr.
APPLICANT: Ford, Ethan E.
TITLE OF INVENTION: RNA Cyclase Ribozymes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,896B
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,857
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 02307E-0700000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular

MOLECULE TYPE: RNA
US-08-431-896B-5
Query Match 66.0%; Score 13.2; DB 1; Length 39;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGTGTCGATCTCCATG 20
Db 22 GGTACTCGAGCTCCATG 5
RESULT 9
US-09-023-228B-36
Sequence 36, Application US/09023228B
Patent No. 6140490
GENERAL INFORMATION:
APPLICANT: BIESECKER, GREGORY
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
TITLE OF INVENTION: COMPLEMENT SYSTEM PROTEINS
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Place #200
CITY: Denver
STATE: Colorado
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,228B
FILING DATE: 12-FEBRUARY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: PCT/US97/01739
FILING DATE: 30 JAN 1997
PRIOR APPLICATION DATA: 08/595,335
APPLICATION NUMBER: 1 FEB 1996
FILING DATE: 1 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson, Esq.
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX50/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-P modified
US-09-023-228B-36
Query Match 66.0%; Score 13.2; DB 3; Length 60;
Best Local Similarity 61.1%; Pred. No. 7.6e+02;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGTGTCGATCTCCATG 20
Db 14 GCGUCUCGAGCUCUAUG 31
RESULT 10
US-09-163-025B-36
Sequence 36, Application US/09163025B

Patent No. 6395888
GENERAL INFORMATION:
APPLICANT: Nexstar Pharmaceuticals, Inc.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: NEX 50 CIP2
CURRENT APPLICATION NUMBER: US/09/163,025B
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 09/023,228
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: PCT/US97/01739
PRIOR FILING DATE: 1997-01-30
NUMBER OF SEQ ID NOS: 198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 60
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Completely
OTHER INFORMATION: Synthesized Nucleic Acid
NAME/KEY: modified base
LOCATION: (1)..(60)
OTHER INFORMATION: All c's and u's are 2'-F
US-09-163-025B-36

Query Match 66.0%; Score 13.2; DB 4; Length 60;
Best Local Similarity 61.1%; Pred. No. 7.6e+02;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGTGTCGATCTCCATG 20
Db 14 GCGUCUCGAGCUCUAUG 31

RESULT 11
US-10-037-282-36
Sequence 36, Application US/10037282
Patent No. 6566343
GENERAL INFORMATION:
APPLICANT: BIESECKER, GREGORY
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF COMPLEMENT SYSTEM
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: NEX 50 CIP 2 CON
CURRENT APPLICATION NUMBER: US/10/037,282
CURRENT FILING DATE: 2002-01-03
PRIOR APPLICATION NUMBER: 09/163,025
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 08/595,335
PRIOR FILING DATE: 1996-02-01
PRIOR APPLICATION NUMBER: PCT/US97/01739
PRIOR FILING DATE: 1997-01-30
NUMBER OF SEQ ID NOS: 198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 60
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
OTHER INFORMATION: all pyrimidines are 2'F
US-10-037-282-36

Query Match 66.0%; Score 13.2; DB 4; Length 60;
Best Local Similarity 61.1%; Pred. No. 7.6e+02;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGTGTCGATCTCCATG 20
Db 14 GCGUCUCGAGCUCUAUG 31

RESULT 12
US-08-431-896B-7
; Sequence 7, Application US/08431896B
; Patent No. 5773244
; GENERAL INFORMATION:
; APPLICANT: Ares, Manuel, Jr.
; APPLICANT: Ford, Ethan E.
; TITLE OF INVENTION: RNA Cyclase Ribozymes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,896B
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,857
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-070000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-431-896B-7

Query Match 66.0%; Score 13.2; DB 1; Length 64;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTGTCGATCTCCATG 20
||| ||||| |||||
Db 33 GGTACCTCGAGCTCCATG 50

RESULT 13
US-08-431-896B-4/c
; Sequence 4, Application US/08431896B
; Patent No. 5773244
; GENERAL INFORMATION:
; APPLICANT: Ares, Manuel, Jr.
; APPLICANT: Ford, Ethan E.
; TITLE OF INVENTION: RNA Cyclase Ribozymes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,896B
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,857
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-070000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-431-896B-4

Query Match 66.0%; Score 13.2; DB 1; Length 66;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTGTCGATCTCCATG 20
||| ||||| |||||
Db 29 GGTACCTCGAGCTCCATG 12

RESULT 14
US-09-209-525-19
; Sequence 19, Application US/09209525
; Patent No. 6303770
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/209,525
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-209-525-19

Query Match 65.0%; Score 13; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTCGATCTCCAT 19
||| ||||| |||||
Db 33 TCTCGATCTCCAT 45

RESULT 15
US-09-311-260-98
; Sequence 98, Application US/09311260
; Patent No. 6214555
; GENERAL INFORMATION:
; APPLICANT: Leushner, James
; APPLICANT: Hui, May
; APPLICANT: Dunn, James M.
; APPLICANT: LaCroix, Jean-Michel
; TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR DETECTION OF
; TITLE OF INVENTION: MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID

;; TITLE OF INVENTION: POLYMERS
;; NUMBER OF SEQUENCES: 189
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppedahl & Larson LLP
;; STREET: P.O. Box 5270
;; CITY: Frisco
;; STATE: CO
;; COUNTRY: US
;; ZIP: 80443-5270
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/311,260
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Larson, Marina T.
;; REGISTRATION NUMBER: 32,038
;; REFERENCE/DOCKET NUMBER: VGEN.P-058-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (970) 668-2050
;; TELEFAX: (970) 668-2082
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 98:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; HYPOTHETICAL: no
;; ANTI-SENSE: no
;; FRAGMENT TYPE: internal
;; US-09-311-260-98

Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TGTCGATCTCCATG 20
| | | | | | | | | |
Db 5 TTCTTGATCTCCATG 20

Search completed: January 28, 2004, 18:43:31
Job time : 92 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:36:28 ; Search time 153 Seconds
(without alignments)
352.868 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 cagggtgtctgcgtatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2667462

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.8	69.0	21	AAV81773	Human SAD PCR prim
C 2	13.8	69.0	41	AAV18872	Primer for rat hyp
C 3	13.8	69.0	63	AAC10340	Human secreted pro
C 4	13.6	68.0	27	ABZ23027	VEE and SIN replic
C 5	13.6	68.0	47	AAZ66728	Human map-related
C 6	13.6	68.0	47	AAZ66820	Human map-related
C 7	13.6	68.0	50	AAZ52340	Primer 28744.p (OL
C 8	13.6	68.0	50	AAZ28444	EGF-like/FGF-8 hom

9	13.6	68.0	50	21	AAA77544	Human PRO214 hybri
10	13.6	68.0	50	21	AAA30035	Probe used in PRO2
11	13.6	68.0	50	22	AAF60355	PRO214 probe #1.
12	13.6	68.0	50	22	AAF72498	Human PRO polypept
13	13.6	68.0	50	23	ABL01039	Human SNP involvin
14	13.6	68.0	50	24	ABK40295	Oligonucleotide pr
15	13.6	68.0	50	25	ACA54898	Secreted and trans
16	13.6	68.0	50	25	ACA58383	Probe #21 used to
17	13.6	68.0	50	25	ACA60090	Human secreted/tra
18	13.6	68.0	50	25	ACA05428	Human secreted pro
19	13.6	68.0	50	25	ABX96107	Human secreted/tra
20	13.6	68.0	50	25	ABX71538	Human secreted/tra
21	13.6	68.0	61	20	AAZ19588	Complement system
22	13.6	68.0	65	24	ABN31465	Rat spliced trans
23	13.6	68.0	65	24	ABN51168	Mouse spliced tran
24	13.4	67.0	21	21	AAZ36007	Forward PCR primer
25	13.4	67.0	26	24	ABZ29883	Candida albicans G
26	13.4	67.0	33	24	ABA04774	F-cassette structu
27	13.4	67.0	41	24	ABA04776	F-cassette structu
28	13.4	67.0	50	24	ABZ01618	Human leukocyte ge
29	13.4	67.0	51	22	AAI78748	Human silent SNP c
30	13.2	66.0	50	24	ABZ04252	Human leukocyte ge
31	13.2	66.0	50	24	AAI50075	Mammalian sialyltr
32	13.2	66.0	51	22	AAI27124	Human SNP oligonuc
33	13.2	66.0	57	22	AAF54785	PCR primer used to
34	13.2	66.0	60	20	AAZ19583	Complement system
35	13.2	66.0	65	24	ABN53230	Mouse spliced tran
36	13.2	66.0	75	22	AAC91193	Portion of Ad5 DNA
37	13	65.0	66	20	AAX80701	Human Zalpha1 cDNA
38	13	65.0	66	24	ABN83098	Human alpha helica
39	13	65.0	66	24	ABK12068	Antisense oligo ZC
40	12.8	64.0	19	22	AAI66133	Human glaucoma-cod
41	12.8	64.0	20	22	AAH03074	Microorganism dete
42	12.8	64.0	40	23	ABK85851	Caspase-3 large su
43	12.8	64.0	40	23	ABK49941	HMFG1/Caspase-3 fu
44	12.8	64.0	40	23	ABK50184	HMFG1 Fab/Caspase-
45	12.8	64.0	47	21	AAZ68616	Human map-related

ALIGNMENTS

RESULT 1
AAV81773/c
ID AAV81773 standard; DNA; 21 BP.

XX AAV81773;
AC AAV81773;
XX 10-MAR-1999 (first entry)
XX Human SAD PCR primer 5284.
DE
XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; PCR primer; ss.

XX Synthetic.
OS Homo sapiens.
XX
PN WO9849317-A2.
XX
PD 05-NOV-1998.
XX
XX 27-APR-1998; 98WO-US08439.
XX 23-OCT-1997; 97US-0063595.
PR 28-APR-1997; 97US-0044428.
PR 20-MAY-1997; 97US-0047222.
PR 11-JUN-1997; 97US-0049477.
PR 11-JUN-1997; 97US-0049756.
PR 18-JUN-1997; 97US-0049914.
XX

PA (SUGE-) SUGEN INC.
XX App H, Clary D, Courtneidge SA, Hui TH, Jallal B;
PI Markby D, Onrust S, Peles E, Plowman GD;
XX WPI; 1999-009434/01.
DR
XX New nucleic acid encoding specific protein tyrosine phosphatases -
PT useful for identifying specific modulators for treatment and
PT prevention of cancer and neurodegenerative disease
XX
XX Example 7; Page 90; 193pp; English.
PS
XX The present invention describes isolated, enriched or purified nucleic
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC above proteins, other than ALK-7, are protein tyrosine phosphatases
CC (PTPs) and are used to identify substances that modulate their activity
CC (i.e. agonists and antagonists, including NBP) in vivo or in vitro.
CC These substances are used to treat or prevent diseases associated with
CC abnormal signal transduction pathways that involve the proteins,
CC particularly cancer (e.g. leukaemia and lymphoma), while modulators of
CC ALK-7 (which is a type I receptor serine/threonine kinase) are used to
CC promote neuronal survival, particularly for treating Alzheimer's,
CC Parkinson's or Huntington's diseases. Nucleic acid fragments of the
CC polynucleotides encoding the proteins can be used as probes to identify
CC and clone related sequences; to detect protein-encoded RNA; to generate
CC transgenic animals and in gene therapy (optionally after mutation). Ab
CC are used to determine the proteins. The present sequence represents a
CC PCR primer for human SAD.
XX
XX Sequence 21 BP; 7 A; 7 C; 5 G; 2 T; 0 other;
SQ
Query Match 69.0%; Score 13.8; DB 20; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 GTGTCTCGATCTCCATG 20
DB 21 GTGTCTGGATCTCCTTG 5
RESULT 2
AAV18872/c
ID AAV18872 standard; DNA; 41 BP.
XX
XX AAV18872;
XX
XX 09-JUL-1998 (first entry)
DT
XX
XX Primer for rat hypocretin 35 cDNA.
DE
XX Rat; hypocretin 35; H35; treatment; neurological disease;
KW homeostatic dysfunction; PCR primer;
KW homeostatic regulatory hormone production; ss.
XX
XX Synthetic.
OS Rattus rattus.
XX
XX WO9805352-A1.
PN
XX
XX 12-FEB-1998.
PD
XX
XX 01-AUG-1997; 97WO-US13657.
PF
XX
XX 02-AUG-1996; 96US-0023220.
PR
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX Bloom FE, Danielson PE, De Lecea L, Foye PE, Gautvik KM;
PI Gautvik VT, Kilduff TS, Sutcliffe JG;
XX
XX WPI; 1998-145352/13.
DR
XX

PT Nucleic acid encoding hypocretin of rat and mouse - useful for
PT diagnosis and treatment of neurological disease, homeostatic
PT dysfunction etc., also sequence for calmodulin kinase-like protein
XX
XX Example 3; Page 73; 111pp; English.
PS
XX The present sequence is a primer for the cDNA encoding rat
CC hypocretin 35 (H35), which is involved in lowering body temperature
CC and reducing food intake.
CC Modulation of the H35 receptor can be used in the treatment of
CC neurological disease or homeostatic dysfunction, or to control
CC homeostatic regulatory hormone production. Hypocretin proteins can
CC be used to raise antibodies (Ab), to identify specific agonists or
CC antagonists, in therapy, to detect Ab and to isolate cognate
CC receptors. Oligonucleotides based on H35 cDNA can be used to detect
CC the hypocretin gene or its RNA transcript, and as antisense agents
CC for inhibiting gene expression. H35 cDNA can also be used for
CC recombinant protein production. The Ab can be used to detect or
CC quantify hypocretin proteins and as a therapeutic inhibitor.
XX
XX Sequence 41 BP; 13 A; 11 C; 6 G; 11 T; 0 other;
SQ
Query Match 69.0%; Score 13.8; DB 19; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 GGTGTCTCGATCTCCAT 19
DB 17 GGTGTCTAGATCTCGAT 1
RESULT 3
AAC10340/c
ID AAC10340 standard; cDNA; 63 BP.
XX
XX AAC10340;
AC
XX 06-OCT-2000 (first entry)
DT
XX Human secreted protein 5' EST, SEQ ID NO: 14415.
DE
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
KW
XX Homo sapiens.
OS
XX EP1033401-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 21-FEB-2000; 2000EP-0200510.
PF
XX
XX 26-FEB-1999; 99US-0122487.
PR
XX
XX (GEST) GENSET.
PA
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX WPI; 2000-500381/45.
DR
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 14415; 71pp + CD-ROM; English.
PS
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX
SQ Sequence 63 BP; 14 A; 14 C; 25 G; 9 T; 1 other;
Query Match 69.0%; Score 13.8; DB 21; Length 63;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GGTGTCGATCTCCAT 19
Db 57 GGTGTCGGGTCCTCCAT 41

RESULT 4
ABZ23027

ID ABZ23027 standard; DNA; 27 BP.

XX
AC ABZ23027;

XX
DT 11-APR-2003 (first entry)

XX
DE VEE and SIN replicon particle chimera related PCR primer SEQ ID NO:35.

XX
KW Chimeric alphavirus; alphavirus replicon particle; vaccine; gene therapy;
KW immune response; gene delivery; structural protein; Sindbis virus; SIN;
KW VEE; venezuelan equine encephalitis virus; PCR primer; ss.

XX
OS Sindbis virus.

OS
OS Venezuelan equine encephalitis virus.

OS
OS Synthetic.

XX
PN WO200299035-A2.

XX
PD 12-DEC-2002.

XX
PF 11-APR-2002; 2002WO-US11585.

XX
PR 31-MAY-2001; 2001US-295451P.

XX
PA (CHIR) CHIRON CORP.

XX
PI Polo J, Perri S, Thudium K;

XX
DR WPI; 2003-140604/13.

XX
PT Novel chimeric alphavirus particle, useful for generating an immune
PT response in a mammal, has RNA derived from one or more alphaviruses,
PT and structural proteins derived from two or more alphaviruses -

XX
PS Example 4; Page 66; 104pp; English.

XX
CC The present invention describes a chimeric alphavirus particle (I),
CC comprising RNA derived from one or more alphaviruses, and structural
CC proteins derived from two or more alphaviruses. Also described is an
CC alphavirus replicon RNA (II) comprising a 5' sequence required for
CC nonstructural protein-mediated amplification, sequences encoding
CC biologically active alphavirus nonstructural proteins, an alphavirus
CC subgenomic promoter, a non-alphavirus heterologous sequence, and a 3'
CC sequence required for nonstructural protein-mediated amplification, where
CC the sequence encoding at least one of the nonstructural proteins is
CC derived from a Biosafety Level 3 (BSL-3) alphavirus and where the
CC sequences of the replicon RNA exhibit sequence identity to at least one
CC third but no more than two-thirds of a genome of a BSL-3 alphavirus. (I)
CC can be used in vaccines and in gene therapy. (I) is useful for generating
CC an immune response in a mammal, by administering (I) to the mammal so
CC generating an immune response. (I) and (II) are useful as gene delivery
CC vehicles having altered cell and tissue tropism, and/or structural

CC protein surface antigenicity. (I) is also useful in the ex vivo and
CC in vivo administration of heterologous genes having therapeutic or
CC prophylactic applications. The present sequence represents a PCR primer
CC which is used in an example from the present invention for the generation
CC of alphavirus replicon particle chimeras with hybrid glycoproteins.

XX
SQ Sequence 27 BP; 8 A; 7 C; 6 G; 6 T; 0 other;

Query Match 68.0%; Score 13.6; DB 25; Length 27;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CAGGTGTCGATCTCCATG 20
Db 7 CAGGGGACTCCATCACCATG 26

RESULT 5

AAZ66728/c

ID AAZ66728 standard; DNA; 47 BP.

XX
AC AAZ66728;

XX
DT 10-SEP-2001 (first entry)

XX
DE Human map-related biallelic marker SEQ ID NO:1075.

XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.

OS
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT variation replace(24,G)

FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

XX
PN WO9954500-A2.

XX
PD 28-OCT-1999.

XX
PF 21-APR-1999; 99WO-IB00822.

XX
PR 21-APR-1998; 98US-0082614.

XX
PR 23-NOV-1998; 98US-0109732.

XX
PA (GEST) GENSET.

XX
PI Cohen D, Blumenfeld M, Chumakov I;

XX
DR WPI; 2000-013267/01.

XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -

XX
PS Claim 1; Page 460; 2745pp; English.

XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.

XX
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297

SQ Sequence 47 BP; 10 A; 15 C; 8 G; 14 T; 0 other;

```
Query Match          68.0%; Score 13.6; DB 21; Length 47;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
```

```

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
/ 1 CAGGTGCTCTCGATCTCCATG 20
    |||||

```

DB Z CAGAIGTATCCATCTGCGATG 21

RESULT 7

ID	AA52340 standard; DNA; 50 BP.
XX	
AC	AA52340;
XX	

DE
XX
Primer 28/44.p (OL1555) use

secreted protein; human; enterocolitis
KW
KW
KW
Zollinger-Ellison syndrome; gastrointestinal ulceration:

KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
 KW anti-thrombotic; wound healing; tissue repair; PCR primer; ss.

XX OS Synthetic

XX
PN
XX

XX
XX
6666T-WFM-67 01

XX
13
13 SEP-1968; 980-0519330.

PR 25-NOV-1997; 97US=0066840.
PR 17-SEP-1997: 97US=0059113

17-SEP-1997: 97US=0059115.
PR
17-SEP-1997: 97US=0059117.
PR

PR 17-SEP-1997: 97US=0059119:
PR 17-SEP-1997: 97US=0059121

PR 17-SEP-1997; 97US=0059184
PR 17-SEP-1997; 97US=0059122;
PR 17-SEP-1997; 97US=0059122;

PK 18-SEP-1997: 37US=0059266
PK 18-SEP-1997: 37US=0059266
PK 18-SEP-1997: 37US=0059266

PK 13-OCT-1997; 37US-0062123;
PK 17-OCT-1997; 97US-0062285;

PR 21-OCT-1997: 97US-0063486;
PR 17-OCT-1997: 97US-0082287;

23-OCT-1997: 37US-0082816;
24-OCT-1997: 37US-0062816;

24-OCT-1997; 97US-0063120.

24-OCT-1997	97US-0063127
24-OCT-1997	97US-0063128
27-OCT-1997	97US-0063329
27-OCT-1997	97US-0063327
28-OCT-1997	97US-0063541
28-OCT-1997	97US-0063542
28-OCT-1997	97US-0063544
28-OCT-1997	97US-0063549
28-OCT-1997	97US-0063550
28-OCT-1997	97US-0063564
29-OCT-1997	97US-0063435
29-OCT-1997	97US-0063704
29-OCT-1997	97US-0063732

29-OCT-1997; 97US-0063738.
29-OCT-1997; 97US-0063738.
29-OCT-1997; 97US-0063734.
29-OCT-1997; 97US-0064215.

29-OCT-1997: 97US-0063735.

PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
XX (GETH) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
PI WPI; 1999-229533/19.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
PT
PT
PS Example 17; Page 128; 320pp; English.
XX
XX Oligonucleotides AAX52276-532 represent PCR primers and probes used
CC to isolate and amplify cDNA encoding secreted and transmembrane human
CC proteins (see AAX52213-74 and AAY13344-403). The cDNA sequences are
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
CC have specific uses based on their homology to known polypeptides,
CC e.g. PRO211 and PRO217 can be used for disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the
CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC microvillus atrophy), skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on
CC cell growth and development, diseases related to growth or survival of
CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
CC polypeptides and portions may have therapeutic applications in wound
CC healing and tissue repair; PRO317 can be used for treating problems of
CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
CC in the heart of genital tract.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;
Query Match 68.0%; Score 13.6; DB 20; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGCTCGATCTCCATG 20
Db 24 CAAGTGCTCGATGTGGATG 43
RESULT 8
AAX28444
ID AAX28444 standard; DNA; 50 BP.
XX
XX AAX28444;
AC
XX
XX 22-JUN-1999 (first entry)
DT
XX
XX EGF-like/FGF-8 homologue coding sequence primer SEQ ID No 62.
DE
XX
XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue; primer;

KW FGF-8 homologue; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9914327-A2.
XX
PD 25-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US18824.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059114.
PR 17-SEP-1997; 97US-0059117.
PR 18-SEP-1997; 97US-0059263.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 24-OCT-1997; 97US-0062816.
PR 29-OCT-1997; 97US-0063704.
XX
PA (GETH) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;
XX
XX WPI; 1999-229532/19.
DR
XX Antibodies against specific proteins overexpressed in tumours
PT
XX
XX Example 1; Page 43; 130pp; English.
XX
XX This sequence represents a primer used to isolate DNA encoding a
CC protein recognised by the antibodies of the invention.
CC The invention relates to antibodies (Ab) that bind to any of the
CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit
CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays, with
CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;
Query Match 68.0%; Score 13.6; DB 20; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGCTCGATCTCCATG 20
Db 24 CAAGTGCTCGATGTGGATG 43
RESULT 9
AAA77544
ID AAA77544 standard; DNA; 50 BP.
XX
XX AAA77544;
AC
XX
XX 07-NOV-2000 (first entry)
DT
XX
XX Human PRO214 hybridisation probe SEQ ID NO:44.
DE
XX
XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine; hybridisation; probe; PCR primer; ss.
XX
XX Homo sapiens.
OS

PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28313.
XX
PR 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 12-JAN-1999; 99US-0115554.
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
PI Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating a cardiovascular, endothelial or
PT angiogenic disorders in mammals -
XX
PS Example 12; Page 122; 315pp; English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating a disorder in mammals by
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PRO expression such as cardiovascular, endothelial or
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC associated with decreased PRO expression. AAA77510 to AAA77721 and
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;
Query Match 68.0%; Score 13.6; DB 21; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGTCTCGATCTCCATG 20
DB 24 CAAGTGTCTCGATGTGGATG 43
RESULT 10
AAA30035
ID AAA30035 standard; DNA; 50 BP.
XX
AC AAA30035;
XX
DT 09-AUG-2000 (first entry)
XX

DE Probe used in PRO214 nucleotide sequence identification.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; HT protein; fibrulin; ADEPT; probe;
KW antibody dependent enzyme mediated prodrug therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200015666-A2.
XX
PD 23-MAR-2000.
XX
XX 08-SEP-1999; 99WO-US20594.
PF
XX 10-SEP-1998; 98US-0099803.
PR 10-SEP-1998; 98WO-US18824.
XX
PA (GETH) GENENTECH INC.
XX
XX Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
PI
XX WPI; 2000-271386/23.
DR
XX New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation -
XX
PS Example 3; Page 75; 200pp; English.
XX
XX This sequence represents a probe used in the identification of the
CC human PRO214 nucleotide sequence. PRO214 shares sequence homology with
CC the HT protein and fibrulin. The invention relates to isolated antibodies
CC which bind to a polypeptide. The "PRO" polypeptides are encoded by genes
CC which are over expressed in the genome of tumour cells. Vectors and host
CC cells comprising the nucleic acid encoding the antibodies are used in the
CC production of the antibodies. The antibodies and nucleic acids encoding
CC them are used for diagnosing a tumour in a mammal. The antibodies are
CC used for inhibiting the growth of tumour cells and identifying compounds
CC that inhibit a biological or immunological activity of and/or expression
CC of a PRO187, PRO533, PRO214, PRO240, PRO211, PRO230, PRO261, PRO246 or
CC PRO317 polypeptide. The antibody can be used in antibody dependent enzyme
CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a
CC prodrug-activating enzyme which converts a prodrug to an anti-cancer
CC drug. The antibodies can be fluorescently labelled and monitored by light
CC microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of
CC tumours.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;
Query Match 68.0%; Score 13.6; DB 21; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGTCTCGATCTCCATG 20
DB 24 CAAGTGTCTCGATGTGGATG 43
RESULT 11
AAF60355
ID AAF60355 standard; DNA; 50 BP.
XX
AC AAF60355;
XX
DT 27-APR-2001 (first entry)
XX
DE PRO214 probe #1.
XX
XX Cytostatic; PRO protein; tumour; cancer; probe; ss.
KW
XX Homo sapiens.
OS
XX WO200105836-A1.
PN


```
XX 25-JAN-2001.
XX
PF 20-DEC-1999; 99WO-US30999.
XX
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX
PA (GETH ) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX WPI; 2001-091968/10.
XX
PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
XX
PS Example 3; Page 92; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is a probe for one such PRO coding sequence. It was
CC found that the PRO genes are amplified in the genome of tumour cells. The
CC gene amplification is expected to be associated with the overexpression
CC of the gene product and contributes to tumorigenesis. Therefore,
CC antagonists of PRO proteins are useful for the treatment of benign or
CC malignant tumours, leukaemias, lymphoid malignancies and other disorders
CC such as neuronal, glial, astrocytal, hypothalamic, glandular, epithelial,
CC inflammatory and immunologic disorders.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 22; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
   |||||
DB 24 CAAGTGTCTCGATGTGGATG 43

RESULT 12
AAF72498
ID AAF72498 standard; DNA; 50 BP.
XX
AC AAF72498;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO polypeptide gene oligonucleotide OLI555.
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US04414.
XX
PR 07-JUL-1999; 99US-0143048.
```

```
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2001-081051/09.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -
XX
PS Example 17; Page 166; 393pp; English.
XX
CC The present sequence is an oligonucleotide used in the isolation of one
CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful for treating skin diseases
CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 22; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
   |||||
DB 24 CAAGTGTCTCGATGTGGATG 43

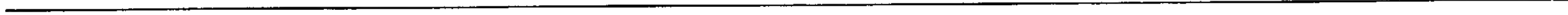
RESULT 13
ABL01039
ID ABL01039 standard; DNA; 50 BP.
XX
AC ABL01039;
XX
XX 05-MAR-2002 (first entry)
XX
DE Human SNP involving a gap oligonucleotide SEQ ID NO:1030.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
XX infection; polymorphic protein; ds.
OS Homo sapiens.
XX
```

PN WO200138586-A2.
XX 31-MAY-2001.
PD 22-NOV-2000; 2000WO-US32311.
XX 24-NOV-1999; 99US-0167383.
XX (CURA-) CURAGEN CORP.
PA Shimkets RA, Leach M;
PI WPI; 2001-355949/37.
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism -
XX
PS Claim 1; Page 559; 674pp; English.
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
XX
SQ Sequence 50 BP; 9 A; 14 C; 17 G; 10 T; 0 other;
Query Match 68.0%; Score 13.6; DB 23; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGTCCTCGATCTCCATG 20
DB 24 CAGGTGTCCTCGATCTCCATG 43
RESULT 14
ABK40295
ID ABK40295 standard; DNA; 50 BP.
XX ABK40295;
AC
XX 15-JUL-2002 (first entry)
DT
XX Oligonucleotide probe for human PRO226 DNA.
DE
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW cytostatic; neuroprotective; probe; ss.
XX
OS Homo sapiens.
XX WO200153486-A1.
PN
XX 26-JUL-2001.
PD
XX 11-FEB-2000; 2000WO-US03565.
PF
XX 08-MAR-1999; 99WO-US05028.
PR

PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
DR
XX Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Example 5; Page 110; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides (AAU86128-AAU86162) and the polynucleotide sequences
CC encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO
CC antibodies are useful for treating benign or malignant tumours
CC (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid
CC malignancies, other disorders such as neuronal, glial, astrocytic,
CC hypothalamic, glandular, macrophagal, stromal and blastocoele disorders,
CC inflammatory, immune and angiogenic disorders. The polynucleotide
CC sequences are also useful in gene therapy. The present sequence
CC represents a probe used in the methods of the present invention.
XX
SQ Sequence 50 BP; 9 A; 10 C; 18 G; 13 T; 0 other;
Query Match 68.0%; Score 13.6; DB 24; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CAGGTGTCCTCGATCTCCATG 20
DB 24 CAGGTGTCCTCGATCTCCATG 43
RESULT 15
ACA54898
ID ACA54898 standard; DNA; 50 BP.
XX ACA54898;
AC
XX 05-JUN-2003 (first entry)
DT
XX Secreted and transmembrane protein associated oligonucleotide #7.
DE
XX Human; secreted and transmembrane protein; gene therapy; psoriasis;
KW enterocolitis; gastrointestinal ulceration; skin disease;
KW keratinocyte differentiation; epithelial cancer; Alzheimer's disease;
KW squamous cell carcinoma; Parkinson's disease; inflammatory disease;
KW amyotrophic lateral sclerosis; rheumatoid arthritis; asthma;
KW multiple sclerosis; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; wound repair; tissue re-growth; ss.
XX
OS Homo sapiens.

Search completed: January 28, 2004, 18:41:49

Job time : 156 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:38:32 ; Search time 1994 Seconds
(without alignments)
243.776 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 cagggtgtctgcattccatg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 306466

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_mam:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	71.0	71	28	BH810806
C 2	13.8	69.0	80	14	H55339
C 3	13.6	68.0	23	28	AZ761953
C 4	13.2	66.0	58	13	BU491208
					BH810806 SALK 0512
					H55339 CHR220278 C
					AZ761953 1M0556K06
					BU491208 604127974

5	13	65.0	55	9	AA907571	AA907571 om09f08.s
6	13	65.0	56	9	AA725701	AA725701 a122b02.s
7	13	65.0	56	9	AA905157	AA905157 ok06a04.s
C 8	12.6	63.0	48	28	AZ800696	AZ800696 2M0058B21
9	12.6	63.0	54	29	CC029869	CC029869 3591_1_11
C 10	12.6	63.0	60	28	AZ425836	AZ425836 1M0206E15
C 11	12.6	63.0	61	9	AI182426	AI182426 uc24h10.r
12	12.6	63.0	70	9	AA578307	AA578307 nl30e12.s
13	12.6	63.0	71	28	AZ323688	AZ323688 1M0045F14
C 14	12.4	62.0	68	28	AZ537585	AZ537585 AST-2P881
15	12.4	62.0	69	14	T12642	T12642 CHR90162 Ch
16	12.2	61.0	60	29	CC249412	CC249412 XF002 Bay
17	12.2	61.0	61	29	AL948303	AL948303 Arabidops
C 18	12.2	61.0	64	10	BF199394	BF199394 SMOV3MCAM
C 19	12.2	61.0	66	28	AZ827039	AZ827039 2M0103O11
20	12.2	61.0	66	28	BH813871	BH813871 SALK 0654
C 21	12.2	61.0	67	9	AA623669	AA623669 vq72c10.s
22	12.2	61.0	68	28	AZ537228	AZ537228 AST-2P030
C 23	12.2	61.0	73	9	AA658373	AA658373 nu22f07.s
24	12.2	61.0	73	12	BJ051979	BJ051979 BJ051979
C 25	12.2	61.0	79	9	AA595959	AA595959 nn66d08.s
C 26	12.2	61.0	79	28	AQ025855	AQ025855 1(2)K0810
27	12.2	61.0	80	10	BE449088	BE449088 ut52c07.Y
28	12	60.0	37	29	CC458682	CC458682 SALK 1216
C 29	12	60.0	39	12	BM280334	BM280334 3'EST-NCD
30	12	60.0	45	28	BH023783	BH023783 BG02336-3
31	12	60.0	50	9	AU103190	AU103190 AU103190
32	12	60.0	50	9	AU104029	AU104029 AU104029
33	12	60.0	50	9	AU105306	AU105306 AU105306
34	12	60.0	59	9	AA082835	AA082835 zn21g12.s
C 35	12	60.0	63	28	AZ379841	AZ379841 1M0135H17
C 36	12	60.0	64	9	AA858284	AA858284 ob13a05.s
C 37	12	60.0	70	9	AI877307	AI877307 vz73e05.r
C 38	12	60.0	70	9	AA237942	AA237942 mx27e04.r
C 39	12	60.0	70	13	BU890908	BU890908 PC43C09 P
C 40	12	60.0	70	14	N84707	N84707 J0579F Huma
C 41	12	60.0	74	13	BU815952	BU815952 N058C05 P
C 42	12	60.0	74	28	AZ615661	AZ615661 1M0445C02
C 43	12	60.0	76	14	H96494	H96494 Yt98g08.r1
44	12	60.0	77	9	AV970179	AV970179 AV970179
C 45	12	60.0	78	14	H38724	H38724 YP62c08.r1

ALIGNMENTS

RESULT 1	BH810806/c	BH810806	71 bp	DNA	linear	GSS 02-MAY-2002
LOCUS	BH810806/c	SALK_051224	Arabidopsis thaliana	TDNA	insertion lines	Arabidopsis
DEFINITION	BH810806	thaliana genomic clone	SALK_051224	genomic survey	sequence.	
ACCESSION	BH810806	BH810806.1	GI:20388624			
VERSION	BH810806	GSS.				
KEYWORDS	BH810806	Arabidopsis thaliana	(thale cress)			
SOURCE	BH810806	Arabidopsis thaliana				
ORGANISM	BH810806	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids				
REFERENCE	BH810806	1 (bases 1 to 71)				
AUTHORS	BH810806	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.				
TITLE	BH810806	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome				
JOURNAL	BH810806	Unpublished				
COMMENT	BH810806	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu				

This is single pass sequence recovered from the left border of

TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .71
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 051224"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
23 a 16 c 16 g 16 t

FEATURES

source

BASE COUNT
ORIGIN

Query Match 71.0%; Score 14.2; DB 28; Length 71;
Best Local Similarity 84.2%; Pred. No. 3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTGTCCTCGATCTCCAT 19
||||| ||||| ||||| |||||
Db 42 CAGGTTTCGTGATCTCCAT 24

RESULT 2

H55339/c

LOCUS

DEFINITION H55339 80 bp mRNA linear EST 07-DEC-1995
CHR220278 Chromosome 22 exon Homo sapiens cDNA clone C22_346 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Buckler AJ
Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Tel: 6177249616
Fax: 6177265736
Email: buckler@helix.mgh.harvard.edu
Seq primer: T3.

FEATURES

source

1. .80
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="C22_346"
/lab_host="E. coli DH5a"
/clone_lib="Chromosome 22 exon"
/note="Vector: pBluescriptPKS+; Site 1: Sal I; Site 2:
Bam HI (destroyed); Exons were isolated from human
Chromosome 22 specific cosmids using a modification of
the method of exon amplification (Proc. Natl. Acad. Sci.
USA 88:4005-4009, 1991). Amplified exons were digested
with Sal I and Bgl II and subsequently cloned into
pBluescriptPKS+ at the Sal I and Bam HI sites."

BASE COUNT
ORIGIN

32 a 15 c 23 g 10 t

Query Match 69.0%; Score 13.8; DB 14; Length 80;
Best Local Similarity 88.2%; Pred. No. 4.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGTGTCCTCGATCTCC 17
||||| ||||| ||||| |||||
Db 32 CAGGTGTCCTTGAGCTCC 16

RESULT 3

AZ761953

LOCUS

DEFINITION AZ761953 23 bp DNA linear GSS 16-FEB-2001
1M0556K06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0556K06 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0556 row: K column: 06

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0556K06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

5 a 7 c 5 g 6 t

BASE COUNT

ORIGIN

Query Match 68.0%; Score 13.6; DB 28; Length 23;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCGATCTCCATG 20
|||||
Db 1 CATGTCCTTGATCTCCAGG 20

RESULT 4

BU491208
LOCUS 58 bp mRNA linear EST 30-NOV-2002
DEFINITION 604127974F1 CSEQRB37 Gallus gallus cDNA clone ChEST950c19 5', mRNA sequence.

ACCESSION BU491208
VERSION BU491208.1 GI:25984785
KEYWORDS EST.
SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken CDNAS

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1..58
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="ChEST950c19"
/sex="Male and female"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRB37"
/note="Organ: pancreas; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT 14 a 10 c 14 g 20 t
ORIGIN

Query Match 66.0%; Score 13.2; DB 13; Length 58;
Best Local Similarity 83.3%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGGTGTCGATCTCCA 18
|||||

Db 28 CAGGTGTGTACATCTCCA 45

RESULT 5

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..55

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1540551"

/lab_host="DH10B"

/clone_lib="Soares NFL T_GBC_S1"

/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 10 c 17 g 18 t

ORIGIN

Query Match 65.0%; Score 13; DB 9; Length 55;

Best Local Similarity 100.0%; Pred. No. 9.2e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGTCTCGATCTCC 17
|||||

Db 41 TGTCTCGATCTCC 53

RESULT 6

AA725701

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1..56

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1540551"

/lab_host="DH10B"

/clone_lib="Soares NFL T_GBC_S1"

/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 10 c 17 g 18 t

ORIGIN

Query Match 65.0%; Score 13; DB 9; Length 55;

Best Local Similarity 100.0%; Pred. No. 9.2e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGTCTCGATCTCC 17
|||||

Db 41 TGTCTCGATCTCC 53

RESULT 6

AA725701

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1..56

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1540551"

/lab_host="DH10B"

/clone_lib="Soares NFL T_GBC_S1"

/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 56)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 789 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .56
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1343499"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTCGGAGCGCGCCCAATTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 9 a 10 c 17 g 20 t
ORIGIN

Query Match 65.0%; Score 13; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGTCTCGATCTCC 17
|||||
Db 42 TGTCTCGATCTCC 54

RESULT 7
AA905157
LOCUS
DEFINITION
IMAGE:1506990 3', similar to gb:U02570 !!! ALU CLASS C WARNING
ENTRY !!! (HUMAN); mRNA sequence.

AA905157 56 bp mRNA linear EST 09-JUN-1998
OK06a04.s1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
IMAGE:1506990 3', similar to gb:U02570 !!! ALU CLASS C WARNING
ENTRY !!! (HUMAN); mRNA sequence.

AA905157
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 56)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 56)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 790 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .56
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1506990"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

BASE COUNT 10 a 10 c 18 g 18 t
ORIGIN

Query Match 65.0%; Score 13; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 9.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGTCTCGATCTCC 17
|||||
Db 42 TGTCTCGATCTCC 54

RESULT 8
AZ800696/c
LOCUS
DEFINITION
clone UUGC2M0058B21 R, genomic survey sequence.

AZ800696 48 bp DNA linear GSS 16-FEB-2001
2M0058B21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0058B21 R, genomic survey sequence.

AZ800696
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 48)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: B column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
1. .48
/organism="Mus musculus"
/mol_type="genomic DNA"

FEATURES
source


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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      18 a   10 c   10 g   10 t
ORIGIN

Query Match      63.0%; Score 12.6; DB 28; Length 48;
Best Local Similarity 78.9%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CAGGTGTCCTCGATCTCCAT 19
        ||||| ||||| |||||
Db      26 CAGGTATCTCGTTAGCCAT 8

RESULT 9
CC029869
LOCUS
DEFINITION
3591_1_113_1_B12.2EL_x_1 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.
ACCESSION
CC029869
VERSION
CC029869.1 GI:29444760
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 54)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3591_1_113_1 column: 9
Class: transposon-tagged.
Location/Qualifiers
1..54
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"

```

```

/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmldb.iastate.edu' and follow the links for 'RescueMu.' Grid P was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
BASE COUNT      10 a   14 c   25 g   5 t
ORIGIN

Query Match      63.0%; Score 12.6; DB 29; Length 54;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 AGGTGTCCTCGATCTCCATG 20
        ||||| ||||| |||||
Db      33 AGGTGTCGCGATGCCACG 51

RESULT 10
AZ425836/c
LOCUS
DEFINITION
AZ425836 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0206E15 F, genomic survey sequence.
ACCESSION
AZ425836
VERSION
AZ425836.1 GI:10549945
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 60)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0206 row: E column: 15
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 60.
Location/Qualifiers
1..60
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0206E15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 25 a 11 c 11 g 13 t
ORIGIN
Query Match 53.0%; Score 12.6; DB 28; Length 60;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AGGTGCTCTCGATCTCCATG 20
Db 20 ATGTTTCTCAATTCCATG 2

RESULT 11
A1182426/c
LOCUS
DEFINITION uc24h10.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1398979 5' similar to TR:Q62433 Q62433 CYTOPLASMIC PROTEIN
NDRI.; mRNA sequence.
A1182426
A1182426.1 GI:3733064
EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 61)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:910695

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .61
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1398979"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/clone lib="Soares mammary gland NbMMG"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGAATGGTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT 13 a 15 c 19 g 14 t
ORIGIN
Query Match 63.0%; Score 12.6; DB 9; Length 61;
Best Local Similarity 78.9%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AGGTGCTCTCGATCTCCATG 20
Db 52 AGCCCTTCGATCTCCAGG 34

RESULT 12
AA578307
LOCUS
DEFINITION AA578307 70 bp mRNA linear EST 12-SEP-1997
nl30el2.s1 NCI CGAP HSC1 Homo sapiens cDNA clone IMAGE:1042222
similar to SW:NDLM HUMAN P03901 NADH-UBIQUINONE OXIDOREDUCTASE
CHAIN 4L.; mRNA sequence.
AA578307
AA578307.1 GI:2356491
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 70)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Donald Orlic, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 282 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .70

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1042222"
/tissue_type="stem cells"
/lab_host="DH10B"
/clone_lib="NCI CGAP HSC1"
/note="Organ: bone marrow; Vector: pAMP10; mRNA made from flow-sorted CD34+/CD38- hematopoietic stem cells, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing

RESULT 15
T12642
LOCUS T12642 69 bp mRNA linear EST 05-JAN-1994
DEFINITION CHR90162 Chromosome 9 exon II Homo sapiens cDNA clone P94_116 5' and 3', mRNA sequence.
ACCESSION T12642
VERSION T12642.1 GI:439391
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 69)
AUTHORS Church,D.M., Stotler,C.J., Rutter,J.L., Murrell,J.R., Trofatter,J.A. and Buckler,A.J.
TITLE Isolation of genes from complex sources of mammalian genomic DNA using exon amplification
JOURNAL Nat. Genet. 6, 98-105 (1994)
MEDLINE 94184375
PUBMED 8136842
COMMENT Contact: Buckler AJ
Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Tel: 6177249616
Fax: 6177265736
Email: buckler@helix.mgh.harvard.edu
Seq primer: T3 and T7.
FEATURES
source
1..69
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="P94_116"
/lab_host="E. coli DH5a"
/clone_lib="Chromosome 9 exon II"
/note="Vector: pBluescriptIIKS; Exons were isolated from human chromosome 9 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with SalI and BamHI and subsequently cloned into pBluescriptIIKS+ at the SalI and BglII sites."
BASE COUNT 15 a 21 c 18 g 15 t
ORIGIN
Query Match 62.0%; Score 12.4; DB 14; Length 69;
Best Local Similarity 92.9%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 TCTCGATCTCCATG 20
||| |||||
Db 3 TCTGGATCTCCATG 16

Search completed: January 28, 2004, 19:41:58
Job time : 2002 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 18:37:54 ; Search time 1494 Seconds
(without alignments)
547.652 Million cell updates/sec

Title: US-09-920-671-80
Perfect score: 20
Sequence: 1 caggtgtctcgatctccatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1459972

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb_ba:
- 2: gb_htg:
- 3: gb_in:
- 4: gb_om:
- 5: gb_ov:
- 6: gb_pat:
- 7: gb_ph:
- 8: gb_pl:
- 9: gb_pr:
- 10: gb_ro:
- 11: gb_sts:
- 12: gb_sy:
- 13: gb_un:
- 14: gb_vi:
- 15: em_ba:
- 16: em_fun:
- 17: em_hum:
- 18: em_in:
- 19: em_mu:
- 20: em_om:
- 21: em_or:
- 22: em_ov:
- 23: em_pat:
- 24: em_ph:
- 25: em_pl:
- 26: em_ro:
- 27: em_sts:
- 28: em_un:
- 29: em_vi:
- 30: em_htg_hum:
- 31: em_htg_inv:
- 32: em_htg_other:
- 33: em_htg_mus:
- 34: em_htg_pln:
- 35: em_htg_rod:
- 36: em_htg_mam:
- 37: em_htg_vrt:
- 38: em_sy:
- 39: em_htgo_hum:
- 40: em_htgo_mus:
- 41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	13.8	69.0	57	9	AF084010	AF084010 Homo sapi
C 2	13.8	69.0	63	6	BD034085	BD034085 Sequence
C 3	13.6	68.0	47	6	AR289340	AR289340 Sequence
C 4	13.6	68.0	47	6	AR289432	AR289432 Sequence
C 5	13.6	68.0	50	6	AX076903	AX076903 Sequence
C 6	13.6	68.0	50	6	AX165835	AX165835 Sequence
C 7	13.6	68.0	50	6	AX201398	AX201398 Sequence
C 8	13.6	68.0	50	6	AX697519	AX697519 Sequence
C 9	13.6	68.0	50	6	BD075458	BD075458 Secretory
C 10	13.6	68.0	50	6	BD172318	BD172318 Secreted
C 11	13.6	68.0	50	6	BD172637	BD172637 Secreted
C 12	13.6	68.0	50	6	BD172956	BD172956 Secreted
C 13	13.6	68.0	50	6	BD173275	BD173275 Secreted
C 14	13.6	68.0	50	6	BD175309	BD175309 Secretory
C 15	13.6	68.0	61	6	AR118196	AR118196 Sequence
C 16	13.6	68.0	61	6	BD130716	BD130716 High-affi
C 17	13.6	68.0	70	7	LAMDRLL137	X70528 Bacterioph
C 18	13.4	67.0	26	6	AX486734	AX486734 Sequence
C 19	13.4	67.0	51	6	AX162361	AX162361 Sequence
C 20	13.2	66.0	39	6	AR013977	AR013977 Sequence
C 21	13.2	66.0	50	6	AX589636	AX589636 Sequence
C 22	13.2	66.0	60	6	AR118191	AR118191 Sequence
C 23	13.2	66.0	60	6	BD130711	BD130711 High-affi
C 24	13.2	66.0	64	6	AR013979	AR013979 Sequence
C 25	13.2	66.0	66	6	AR013976	AR013976 Sequence
C 26	13	65.0	66	6	AR173253	AR173253 Sequence
C 27	13	65.0	66	6	BD087206	BD087206 Mammalian
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C 29	12.8	64.0	47	6	AR291001	AR291001 Sequence
C 30	12.8	64.0	47	6	AR291230	AR291230 Sequence
C 31	12.8	64.0	50	6	AX613046	AX613046 Sequence
C 32	12.8	64.0	60	6	AX601350	AX601350 Sequence
C 33	12.8	64.0	60	6	BD180765	BD180765 Array of
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C 35	12.6	63.0	21	6	AR067340	AR067340 Sequence
C 36	12.6	63.0	24	6	AX743920	AX743920 Sequence
C 37	12.6	63.0	25	6	AX613481	AX613481 Sequence
C 38	12.6	63.0	26	6	I28831	I28831 Sequence 67
C 39	12.6	63.0	27	6	AR150679	AR150679 Sequence
C 40	12.6	63.0	27	6	E16228	E16228 Primer. 7/1
C 41	12.6	63.0	27	6	E27240	E27240 Novel physi
C 42	12.6	63.0	27	6	E28312	E28312 Utilization
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ALIGNMENTS

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ACCESSION AF084010
VERSION AF084010.1 GI:4836183
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 57)
AUTHORS Pachman,L.M., Liotta,M.R., Caliendo,J., Greene,M., Pope,R.M.,
Morrelo,F., Lawton,T., Crawford,S., Wu,T.T. and O'Gorman,M.R.G.
TITLE New Onset Juvenile Dermatomyositis: Muscle Biopsy

Pred. No. is the number of results predicted by chance to have a

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SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE						
AUTHORS	Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I.					
TITLE	Polypeptidic compositions and methods for the treatment of tumors					
JOURNAL	Patent: WO 0105836-A 15 25-JAN-2001;					
	Genentech, Inc. (US)					
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LOCUS	AX165835	Sequence 1030 from Patent WO0138586.	50 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	AX165835	Sequence 1030 from Patent WO0138586.	50 bp	DNA	linear	PAT 22-JUN-2001
ACCESSION	AX165835	Sequence 1030 from Patent WO0138586.	50 bp	DNA	linear	PAT 22-JUN-2001
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SOURCE		Homo sapiens				
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REFERENCE						
AUTHORS	Shinkets,R.A. and Leach,M.					
TITLE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof					
JOURNAL	Patent: WO 0138586-A 1030 31-MAY-2001;					
	Curagen Corporation (US)					
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BD075458
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD075458
Secretory and transmembrane polypeptide and nucleic acid encoding the same.
BD075458
JP 2001516580-A/91
synthetic construct
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artificial sequences.
1 (bases 1 to 50)
Wood, W.I., Gurney, A.L., Goddard, A., Penica, D., Chen, J. and Yuan, J.
Secretory and transmembrane polypeptide and nucleic acid encoding the same
Patent: JP 2001516580-A 91 02-OCT-2001;
GENENTECH INC
OS Artificial Sequence
PN JP 2001516580-A/91
PD 02-OCT-2001
PF 16-SEP-1998 JP 2000511867
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI
JEAN CHEN,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/00,
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Best Local Similarity 80.0%; Pred. No. 2.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD172318
Secreted and transmembrane polypeptides and nucleic acids encoding the same.
BD172318
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artificial sequences.
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Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.
Secreted and transmembrane polypeptides and nucleic acids encoding the same
Patent: JP 2002223786-A 91 13-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002223786-A/91
PD 13-AUG-2002
PF 18-DEC-2001 JP 2001385135
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PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
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KEYWORDS	JP 2002238586-A/91.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 50)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238586-A 91 27-AUG-2002;		
COMMENT	GENENTECH INC		
OS	Artificial Sequence		
PN	JP 2002238586-A/91		
PD	27-AUG-2002		
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI			
JIAN ZHENG,			
PI JEAN YUAN			
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KEYWORDS	JP 2002238587-A/91.		
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ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 50)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238587-A 91 27-AUG-2002;		
COMMENT	GENENTECH INC		
OS	Artificial Sequence		
PN	JP 2002238587-A/91		
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24-NOV-1997 US	60/066453,25-NOV-1997 US 60/066840 PI		
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI			
JIAN ZHENG,			
PI JEAN YUAN			
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21,PC			
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DEFINITION
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Secretory and transmembrane polypeptide and nucleic acid encoding
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ACCESSION
BD175309.1 GI:29121005
VERSION
JP 2002253280-A/91.
KEYWORDS
synthetic construct
SOURCE
artificial sequences.
ORGANISM
1 (bases 1 to 50)
REFERENCE
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
AUTHORS
Secretory and transmembrane polypeptide and nucleic acid encoding
the same
TITLE
Patent: JP 2002253280-A 91 10-SEP-2002;
JOURNAL
GENENTECH INC
COMMENT
OS Artificial Sequence
PN JP 2002253280-A/91
PD 10-SEP-2002
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
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PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,
PC C12R1:91),
PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC

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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGGTGTCTCGATCTCCATG 20
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RESULT 15
AR118196
LOCUS AR118196 61 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 41 from patent US 6140490.
ACCESSION AR118196
VERSION AR118196.1 GI:14099102
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 61)
AUTHORS Biesecker, G. and Gold, L.
TITLE High affinity nucleic acid ligands of complement system proteins
JOURNAL Patent: US 6140490-A 41 31-OCT-2000;
FEATURES Location/Qualifiers
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QY 1 CAGGTGTCTCGATCTCCATG 20
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Search completed: January 28, 2004, 19:08:29
Job time : 1500 secs